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Key indicators

Single-crystal X-ray study T = 295 KMean $\sigma(C-C) = 0.004 \text{ Å}$ R factor = 0.064 wR factor = 0.141 Data-to-parameter ratio = 15.7

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

4-(5-Chloro-2-hydroxybenzylideneamino)-1,5dimethyl-2-phenyl-1*H*-pyrazol-3(2*H*)-one

The title Schiff base compound, $C_{18}H_{16}ClN_3O_2$, has been synthesized by the reaction of 4-amino-1,5-dimethyl-2-phenyl-1,2-dihydropyrazol-3-one and 5-chloro-2-hydroxybenzaldehyde in MeOH solution. As expected, the compound adopts an *E* configuration about the imine C=N bond. The N atom is also involved in an intramolecular O-H···N bond which stabilizes the configuration. Intramolecular hydrogen bonds and intermolecular C-H···O interactions are observed.

Comment

The background to this study is described in a preceding paper (Sun, 2006). As an extension of our work (Sun, Xie *et al.*, 2006; Sun, Zhang, Jin *et al.*, 2006); Sun, Zhang, Wang *et al.*, 2006) on the structural characterization of antipyrine derivatives, a new Schiff base compound, (I), is reported here.



The molecular structure of (I) is illustrated in Fig. 1. All the bond distances and angles are in normal ranges (Allen *et al., 1987*) and comparable to those observed in similar antipyrine Schiff bases cited above. The C12—N3 bond length of 1.281 (3) Å is as expected for a normal imine double bond. Because of conjugation through this imino double bond, the N1/N2/C7/C8/C9 pyrazoline and C13–C18 benzene rings are nearly coplanar [dihedral angle 1.5 (3)°]. As expected, the



Figure 1

The molecular structure of (I), showing 30% probability displacement ellipsoids and the atom-numbering scheme. The $O-H\cdots N$ and $C-H\cdots O$ hydrogen bonds are shown as dashed lines.

© 2006 International Union of Crystallography All rights reserved Received 9 November 2006 Accepted 17 November 2006 molecular structure of the Schiff base adopts an E configuration about the imine C12-N3 bond, as in the other similar antipyrine derivatives that have been reported. In the structure of (I) an intramolecular O-H···N hydrogen bond involving hydroxyl atom O2 and imine atom N3 and another intramolecular C-H···O hydrogen bond involving the C12/ H12 group and carbonyl atom O1 stabilize the E configuration about the imine C=N bond (Table 1).

A packing diagram of (I) is shown in Fig. 2. In the crystal structure, molecules interact through intermolecular C- $H \cdots O$ hydrogen bonds.

Experimental

All the chemicals were obtained from commercial sources and used without purification. 4-Amino-1,5-dimethyl-2-phenyl-1,2-dihydropyrazol-3-one (0.2 mmol, 40.6 mg) and an equimolar quantity of 5chloro-2-hydroxybenzaldehyde (0.2 mmol, 31.3 mg) were dissolved in methanol (20 ml). The mixture was stirred for 30 min at room temperature to give a clear yellow solution. This solution was kept in air for 8 d, after which time yellow needle-shaped crystals of (I) were formed at the bottom of the vessel on slow evaporation of the methanol (yield 93.6%). Analysis calculated for C₁₈H₁₆ClN₃O₂: C 63.25, H 4.72, N 12.29%; found: C 63.13, H 4.74, N 12.23%.

Z = 4

 $D_x = 1.358 \text{ Mg m}^{-3}$

0.45 \times 0.11 \times 0.01 mm

3447 independent reflections

Mo $K\alpha$ radiation

 $\mu = 0.24 \text{ mm}^{-1}$

T = 295 (2) K

Needle, vellow

Crystal data

C18H16CIN3O2 $M_r = 341.79$ Monoclinic, $P2_1/c$ a = 4.948 (1) Åb = 23.931 (2) Å c = 14.294 (1) Å $\beta = 99.107 \ (1)^{\circ}$ V = 1671.3 (2) Å³

Data collection

Bruker APEX area-detector 13419 measured reflections diffractometer and a scans 2333 reflections with $I > 2\sigma(I)$ Absorption correction: multi-scan $R_{\rm int} = 0.046$ $\theta_{\rm max} = 26.5^\circ$ (SADABS; Sheldrick, 1996) $T_{\rm min}=0.967,\ T_{\rm max}=0.998$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0445P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.064$	+ 0.7061P]
$wR(F^2) = 0.141$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.09	$(\Delta/\sigma)_{\rm max} = 0.001$
3447 reflections	$\Delta \rho_{\rm max} = 0.18 \text{ e} \text{ Å}^{-3}$
220 parameters	$\Delta \rho_{\rm min} = -0.25 \text{ e } \text{\AA}^{-3}$
H-atom parameters constrained	

Table 1

Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D - \mathbf{H} \cdots A$
O2−H2···N3	0.82	1.86	2.589 (3)	148
C12-H12···O1	0.93	2.40	3.067 (3)	128
$C6-H6\cdots O1^i$	0.93	2.55	3.425 (4)	156
$C10-H10C\cdots O1^{ii}$	0.96	2.51	3.467 (4)	172
$C15{-}H15{\cdots}O2^{iii}$	0.93	2.53	3.435 (4)	163

Symmetry codes: (i) x - 1, y, z; (ii) $x, -y + \frac{3}{2}, z - \frac{1}{2}$; (iii) -x + 1, -y + 1, -z.



Figure 2

The crystal packing of (I), viewed down the *a* axis. All $O-H \cdots N$ and C-H···O hydrogen bonds are shown as dashed lines.

All H atoms were positioned geometrically (O-H = 0.82 Å and C-H = 0.93 or 0.96 Å) and constrained to ride on their parent atoms with $U_{iso}(H) = 1.5U_{eq}(O)$, $U_{iso}(H) = 1.2U_{eq}(C)$ for $Csp^2 H$ atoms or $U_{\rm iso}({\rm H}) = 1.5 U_{\rm eq}({\rm C})$ for methyl H atoms.

Data collection: SMART (Bruker, 2002); cell refinement: SAINT-Plus (Bruker, 2002); data reduction: SAINT-Plus; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL (Bruker, 2002); software used to prepare material for publication: SHELXTL.

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